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Figure 1

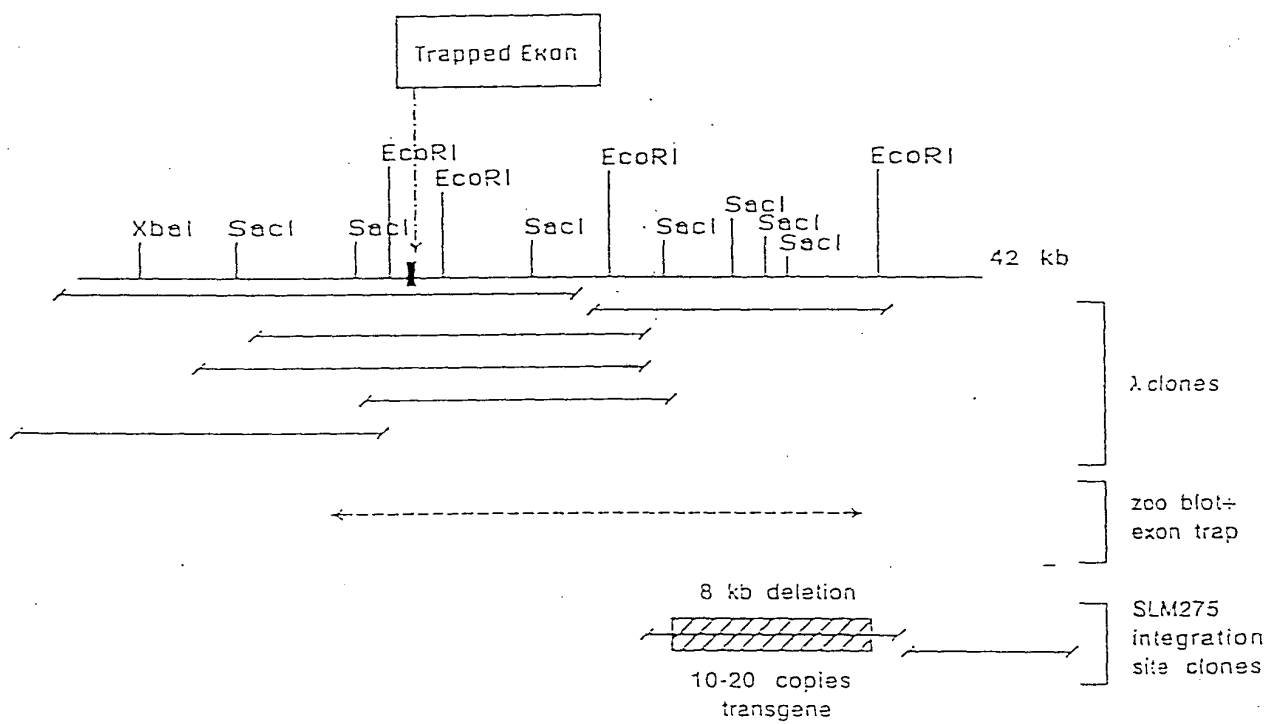


Figure 2

166.	167.	168.	169.	170.	171.	172.	173.	174.	175.	176.	177.	178.	179.	180.	181.	182.	183.	184.	185.	186.	187.	188.	189.	190.	191.	192.	193.	194.	195.	196.	197.	198.	199.	200.	201.	202.	203.	204.	205.	206.	207.	208.	209.	210.	211.	212.	213.	214.	215.	216.	217.	218.	219.	220.	221.	222.	223.	224.	225.	226.	227.	228.	229.	230.	231.	232.	233.	234.	235.	236.	237.	238.	239.	240.	241.	242.	243.	244.	245.	246.	247.	248.	249.	250.	251.	252.	253.	254.	255.	256.	257.	258.	259.	260.	261.	262.	263.	264.	265.	266.	267.	268.	269.	270.	271.	272.	273.	274.	275.	276.	277.	278.	279.	280.	281.	282.	283.	284.	285.	286.	287.	288.	289.	290.	291.	292.	293.	294.	295.	296.	297.	298.	299.	300.	301.	302.	303.	304.	305.	306.	307.	308.	309.	310.	311.	312.	313.	314.	315.	316.	317.	318.	319.	320.	321.	322.	323.	324.	325.	326.	327.	328.	329.	330.	331.	332.	333.	334.	335.	336.	337.	338.	339.	340.	341.	342.	343.	344.	345.	346.	347.	348.	349.	350.	351.	352.	353.	354.	355.	356.	357.	358.	359.	360.	361.	362.	363.	364.	365.	366.	367.	368.	369.	370.	371.	372.	373.	374.	375.	376.	377.	378.	379.	380.	381.	382.	383.	384.	385.	386.	387.	388.	389.	390.	391.	392.	393.	394.	395.	396.	397.	398.	399.	400.	401.	402.	403.	404.	405.	406.	407.	408.	409.	410.	411.	412.	413.	414.	415.	416.	417.	418.	419.	420.	421.	422.	423.	424.	425.	426.	427.	428.	429.	430.	431.	432.	433.	434.	435.	436.	437.	438.	439.	440.	441.	442.	443.	444.	445.	446.	447.	448.	449.	450.	451.	452.	453.	454.	455.	456.	457.	458.	459.	460.	461.	462.	463.	464.	465.	466.	467.	468.	469.	470.	471.	472.	473.	474.	475.	476.	477.	478.	479.	480.	481.	482.	483.	484.	485.	486.	487.	488.	489.	490.	491.	492.	493.	494.	495.	496.	497.	498.	499.	500.	501.	502.	503.	504.	505.	506.	507.	508.	509.	510.	511.	512.	513.	514.	515.	516.	517.	518.	519.	520.	521.	522.	523.	524.	525.	526.	527.	528.	529.	530.	531.	532.	533.	534.	535.	536.	537.	538.	539.	540.	541.	542.	543.	544.	545.	546.	547.	548.	549.	550.	551.	552.	553.	554.	555.	556.	557.	558.	559.	560.	561.	562.	563.	564.	565.	566.	567.	568.	569.	570.	571.	572.	573.	574.	575.	576.	577.	578.	579.	580.	581.	582.	583.	584.	585.	586.	587.	588.	589.	590.	591.	592.	593.	594.	595.	596.	597.	598.	599.	600.	601.	602.	603.	604.	605.	606.	607.	608.	609.	610.	611.	612.	613.	614.	615.	616.	617.	618.	619.
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[illegible]

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Figure 3A

10	20	30	40	50	60
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
EcoRI	HpaI				
GAATTCGGT	TAACTGAGGA	CAAAGGGTAA	TGCAGAAGTG	ATATTTGATT	TCCATTCTCA 60
		DraI			
TTCCCACTGG	CCTTGATATT	TAAACTGATT	CCTGCCACCA	GGTCCTTGGG	CCACCCTGTC 120
	Esp3I	SphI			
CCTGCGTCTC	ATATTTCTGC	ATGCTGCTTT	GTTTGTATAT	AGTGCGCTCC	TGGCCTCAGG 180
CTCGCTCCCC	TCCAGCTCTC	GCTTCACTGT	TCTCCAAGTC	AGAAGCCCCC	GCATCCGCCG 240
			BssHII		
CGCAGCAGCG	TGAGCCGTAG	TCACTGCTGG	CCGCTTCGCC	TGCGTGCGCG	CACGGAAATC 300
GGGGAGCCAG	GAACCCAAGG	AGCCGCCGTC	CGCCCGCTGT	GCCTCTGCTA	GACCACTCGC 360
AGCCCCAGCC	TCTCTCAAGC	GCACCCACCT	CCGCGCACCC	CAGCTCAGGC	GAAGCTGGAG 420
TGAGGCTGAA	TCACCCCTTC	TCTAGGGCCA	CCACTCTTTT	ATCGCCCTTC	CCAAGATTTG 480

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Figure 33

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
<p>Eco47III AatII</p> <p>AGAAGCGCTG CCGGAGGAAA GACGTCCTCT TGATCTCTGA CAGGCGGGG TTTACTGCTG 540</p>						
<p>BssHII</p> <p>PstI</p> <p>TCCTGCAGGC GCGCCTCGCC TACTGTGCC TCCGCTACGA CCCCAGACCA GCCCAGGTCA 600</p>						
<p>BspHI</p> <p>CGTCCGTGAG AAGGGATCAT GAAGCACTTG GTAGCAGCCT GCCTTTTGGT TGGACTCAGC 650</p> <p>M K H L V A A W L L V G L S</p>						
<p>CTCGGGGTGC CCCAGTTCGG CAAAGGTGAC ATTTGCAACC CGAACCCTG TGAAAATGGT 720</p> <p>L G V P Q F G K G D I C N P N P C E N G</p>						
<p>BspMI</p> <p>GGCATCTGTC TGTCAGGACT GGCTGATGAT TCCTTTTCCT GTGAGTGTCC AGAAGGCTTC 780</p> <p>G I C L S G L A D D S F S C E C P E G F</p>						
<p>BspMI</p> <p>GCAGGTCCGA ACTGCTCTAG TGTTGTGGAG GTTGCATCAG ATGAAGAAAA GCCTACTTCA 840</p> <p>A G P N C S S V V E V A S D E E K P T S</p>						
<p>GCAGGTCCCT GCATCCCTAA CCCATGCCAT AACGGAGGAA CCTGTGAGAT AAGCGAAGCC 900</p> <p>A G P C I P N P C H N G G T C E I S E A</p>						
<p>TATCGAGGAG ACACATTCAT AGGCTATGTT TGTAATGTC CTCGGGGATT TAATGGGATT 960</p> <p>Y R G D T F I G Y V C K C P E G F N G I</p>						

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Figure 3c

10	20	30	40	50	60
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CACTGTCAGC ACAATATAAA TGAATGTGAA GCTGAGCCTT GCAGAAATGG CGGAATATGT 1020
H C Q H N I N E C E A E P C R N G G I C

BsmI
ACCGACCTTG TTGCTAACTA CTCTTGTGAA TGCCCGAGGAG AATTTATGGG ACGAAATTGT 1080
T D L V A N Y S C E C P G E F M G R N C

CAATATAAAT GCTCTGGGCA CTTGGGAATC GAAGGTGGGA TCATATCTAA TCAGCAAATC 1140
Q Y K C S G H L G I E G G I I S N Q Q I

SacI
Ecl1136II
ACAGCTTCAT CTAATCACCG AGCTCTTTT GGAATCCAGA AGTGGTATCC CTACTATGCT 1200
T A S S N H R A L F G L Q K W Y P Y Y A

NcoI
MscI
BclI
PvuII
CGACTTAATA AGAAGGGCCT TATAAATGCC TGGACAGCTG CTGAAATGA CAGATGGCCA 1260
R L N K K G L I N A W T A A E N D R W P

TGGATTCAGA TAAATTTGCA AAGAAAAATG AGAGTCACTG GTGTTATTAC CCAAGGAGCA 1320
W I Q I N L Q R K M R V T G V I T Q G A

AAAAGGATTG GAAGCCCGAGA GTACATAAAA TCCTACAAAA TTGCCTACAG CAATGACGGG 1380
K R I G S P E Y I K S Y K I A Y S N D G

BbsI
EaeI
AAACACCTGGG CAATGTACAA AGTAAAAGGC ACCAATGAAG AGATGGTCTT TCGTGGAAAT 1440
K T W A M Y K V K G T N E E M V P R G N

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Figure 3D

10 20 30 40 50 60
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

NdeI

GTTGATAACA ACACACCATA TGCTAATTCT TTCACACCCC CAATCAAAGC TCAGTATGTA 1500
V D N N T P Y A N S F T P P I K A Q Y V

AGACTCTACC CCCAAATTG TCGAAGGCAT TGTACTTTAA GAATGGAAC TCTTGGCTGT 1550
R L Y P Q I C R R H C T L R M E L L G C

SacI
Ecl135II

GAGCTCTCAG GCTGTTTCAGA ACCTTGGGG ATGAAATCAG GGCATATACA AGACTACCAG 1620
E L S G C S E P L G M K S G H I Q D Y Q

BbsI

ATCACTGCCT CCAGCGTCTT CAGAACACTC AACATGGACA TGTTTACTTG GGAACCAAGG 1680
I T A S S V F R T L N M D M F T W E P R

AAAGCCAGGC TGGACAAGCA AGGCAAGTA AATGCCTGGA CTTCCGGCCA TAACGACCAG 1740
K A R L D K Q G K V N A W T S G H N D Q

TCACAATGGT TACAGGTTGA TCTTCTTGTC CCTACTAAGG TGACAGGCAT CATTACACAA 1800
S Q W L Q V D L L V P T K V T G I I T Q

PmlI

GGAGCTAAG ATTTTGGTCA CGTGCAGTTT GTTGGGTCAT ACAACTAGC TTACAGCAAT 1860
G A K D F G H V Q F V G S Y K L A Y S N

ApaLI

GATGGAGAAC ACTGGATGGT GCACCAGGAT GAAAPACAGA GGAAAGACAA GCTTTTTCAA 1920
D G E H W M V H Q D E K Q R K D K V F Q

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Figure 3E

10	20	30	40	50	60
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

GGCAATTTTG ACAATGACAC TCACAGGAAA AATGTCATCG ACCCTCCCAT CTATGCACGA 1980
G N F D N D T H R K N V I D P P I Y A R

TTCATAAGAA TCCTTCCTTG GTCCTGGTAT GGAAGSATCA CTCTGCGGTC AGAGCTGCTG 2040
F I R I L P W S W Y G R I T L R S E L L

FspI

GGCTGCGCAG AGGAGGAATG AAGTGGGGG CCGCACATCC CACAATGCTT TTCTTTATTT 2100
G C A E E E

TCCTATAAT ATCTCCACGA AATGAAGTGT GTGAAGCTGA TGGAACTGC ATTTGTTTTT 2160

HindIII

TTCAAAGTGT TCAAATTATG GTAGGCTACT GACTGTCTTT TTAGGAGTTC TAAGCTTGCC 2220

TTTTTAATAA TTTAATTGG TTTCCTTGC TCAACTCTCT TATGTAATAT CAACTGTCT 2280

EcoRI

GTGAGTACT CTTCTTGTTC TCT 2303

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Figure 4A

5'	TCT	CTT	9 TAG	TCA	CCA	18 CTC	TCG	CCC	27 TCT	CCA	AGA	36 ATT	TGT	TTA	45 ACA	AAG	CGC	54 TGA
	S	L	*	S	P	L	S	P	S	P	R	I	C	L	T	K	R	*
	GGA	AAG	63 AGA	ACG	TCT	72 TCT	TGA	ATT	81 CTT	TAG	TAG	90 GGG	CGG	ACT	99 CTG	CTG	CTG	108 CCC
	G	K	R	T	S	S	*	I	L	*	*	G	R	S	L	L	L	P
	TGC	GCT	117 GCC	ACC	TCG	126 GCT	ACA	CTG	135 CCC	TCC	GCG	144 ACG	ACC	CCT	153 GAC	CAG	CCG	162 GGG
	C	A	A	T	S	A	T	L	P	S	A	T	T	P	D	Q	P	G
	TCA	CGT	171 CCG	GGA	GAC	180 GGG	ATC	ATG	189 AAG	CGC	TCG	198 GTA	GCC	GTC	207 TGG	CTC	TTG	216 GTC
	S	R	P	G	D	G	I	M	K	R	S	V	A	V	W	L	L	V
	GGG	CTC	225 AGC	CTC	GGT	234 GTC	CCC	CAG	243 TTC	GGC	AAA	252 GGT	GAT	ATT	261 TGT	GAT	CCC	270 AAT
	G	L	S	L	G	V	P	Q	F	G	K	G	D	I	C	D	P	N
	CCA	TGT	279 GAA	AAT	GGA	288 GGT	ATC	TGT	297 TTG	CCA	GGA	306 TTG	GCT	GTA	315 GGT	TCC	TTT	324 TCC
	P	C	E	N	G	G	I	C	L	P	G	L	A	V	G	S	F	S
	TGT	GAG	333 TGT	CCA	GAT	342 GGC	TTC	ACA	351 GAC	CCC	AAC	360 TGT	TCT	AGT	369 GTT	GTG	GAG	378 GTT
	C	E	C	P	D	G	F	T	D	P	N	C	S	S	V	V	E	V
	GCA	TCA	387 GAT	GAA	GAA	396 GAA	CCA	ACT	405 TCA	GCA	GCT	414 CCC	TGC	ACT	423 CCT	AAT	CCA	432 TGC
	A	S	D	E	E	E	P	T	S	A	G	P	C	T	P	N	P	C
	CAT	AAT	441 GGA	GGA	ACC	450 TGT	GAA	ATA	459 AGT	GAA	GCA	468 TAC	CGA	GGG	477 GAT	ACA	TTC	486 ATA
	H	N	G	G	T	C	E	I	S	E	A	Y	R	G	D	T	F	I
	GGC	TAT	495 GTT	TGT	AAA	504 TGT	CCC	CGA	513 GGA	TTT	AAT	522 GGG	ATT	CAC	531 TGT	CAG	CAC	540 AAC
	G	Y	V	C	K	C	P	R	G	F	N	G	I	H	C	Q	H	N
	ATA	AAT	549 GAA	TGC	GAA	558 GTT	GAG	CCT	567 TGC	AAA	AAT	576 GGT	GGA	ATA	585 TGT	ACA	GAT	594 CTT
	I	N	E	C	E	V	E	P	C	K	N	G	G	I	C	T	D	L
	GTT	GCT	603 AAC	TAT	TCC	612 TGT	GAG	TGC	621 CCA	GGC	GAA	630 TTT	ATG	GGA	639 AGA	AAT	TGT	648 CAA
	V	A	N	Y	S	C	E	C	P	G	E	F	M	G	R	N	C	Q

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Figure 4B

TAC	AAA	657	TGC	TCA	GGC	655	CCA	CTG	GGA	575	ATT	GAA	GGT	634	GGA	ATT	ATA	693	TCA	AAC	CAG	702	CAA
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Y	K	C	S	G	P	L	G	I	E	G	G	I	I	S	N	Q	Q						
ATC	ACA	711	GCT	TCC	TCT	ACT	CAC	CGA	GCT	729	CTT	TTT	GGA	CTC	CAA	747	AAA	TGG	TAT	CCC			
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I	T	A	S	S	T	H	R	A	L	F	G	L	Q	K	W	Y	P						
TAC	TAT	765	GCA	CGT	CTT	AAT	AAG	AAG	GGG	783	CTT	ATA	AAT	GGC	TGG	801	ACA	GCT	CCA	GAA			
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Y	Y	A	R	L	N	K	K	G	L	I	N	A	W	T	A	A	E						
AAT	GAC	819	AGA	TGG	AAC	CGG	TGG	ATT	CAG	837	ATA	AAT	TTG	CAA	AGA	855	AAA	ATG	AGA	GTT			
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N	D	R	W	N	R	W	I	Q	I	N	L	Q	R	K	M	R	V						
ACT	GST	873	GTG	ATT	ACC	CAA	GGG	GCC	AAG	891	AGG	ATT	GGA	AGC	CCA	909	GAG	TAT	ATA	AAA			
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T	G	V	I	T	Q	G	A	K	R	I	G	S	P	E	Y	I	K						
TTC	TAC	927	AAA	ATT	GCC	TAC	AGT	AAT	GAT	945	GGA	AAG	ACT	TGG	GCA	953	ATG	TAC	AAA	GTC			
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F	Y	K	I	A	Y	S	N	D	G	K	T	W	A	M	Y	K	V						
AAA	GCC	981	ACC	AAT	GAA	GAC	ATG	GTG	TTT	999	CGT	GGA	AAC	ATT	GAT	1017	AAC	AAC	ACT	CCA			
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K	G	T	N	E	D	M	V	F	R	G	N	I	D	N	N	T	P						
TAT	GCT	1035	AAC	TCT	TTC	ACA	CCC	CCC	ATA	1053	AAA	GCT	CAG	TAT	GTA	1071	AGA	CTC	TAT	CCC			
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Y	A	N	S	F	T	P	P	I	K	A	Q	Y	V	R	L	Y	P						
CAA	GTT	1089	TGT	CGA	AGA	CAT	TGC	ACT	TTG	1107	CGA	ATG	GAA	CTT	CTT	1125	GGC	TGT	GAA	CTG			
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Q	V	C	R	R	H	C	T	L	R	M	E	L	L	G	C	E	L						
TCG	GST	1143	TGT	TCT	GAG	CCT	CTG	GCT	ATG	1151	AAA	TCA	GGA	CAT	ATA	1179	CAA	GAC	TAT	CAG			
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S	G	C	S	E	P	L	G	M	K	S	G	H	I	Q	D	Y	Q						
ATC	ACT	1197	GCC	TCC	AGC	ATC	TTC	AGA	ACG	1215	CTC	AAC	ATG	GAC	ATG	1233	TTC	ACT	TGG	GAA			
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I	T	A	S	S	I	F	R	T	L	N	M	D	M	F	T	W	E						
CCA	AGG	1251	AAA	GCT	CGG	CTG	GAC	AAG	CAA	1259	GGC	AAA	GTG	AAT	GCC	1267	TGG	AOC	TCT	GCC			
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P	R	K	A	R	L	D	K	Q	G	K	V	N	A	W	T	S	G						
CAC	AAT	1305	GAC	CAG	TCA	CAA	TGG	TTA	CAG	1323	GTG	GAT	CTT	CTT	GTT	1341	CCA	ACC	AAA	GTG			
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H	N	D	Q	S	Q	W	L	Q	V	D	L	L	V	P	T	K	V						

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Figure 4c

1359	1368	1377	1386	1395	1404
ACT GGC ATC ATT ACA CAA GCA GCT AAA GAT TTT GGT CAT GTA CAG TTT GTT GGC					
T G I I T Q G A K D F G H V Q F V G					
1413	1422	1431	1440	1449	1458
TCC TAC AAA CTG GCT TAC AGC AAT GAT GGA GAA CAC TGG ACT GTA TAC CAG GAT					
S Y K L A Y S N D G E H W T V Y Q D					
1467	1476	1485	1494	1503	1512
GAA AAG CAA AGA AAA GAT AAG GTT TTC CAG GGA AAT TTT GAC AAT GAC ACT CAC					
E K Q R K D K V F Q G N F D N D T H					
1521	1530	1539	1548	1557	1566
ACA AAA AAT CTC ATC GAC CCT CCC ATC TAT GCA CGA CAC ATA AGA ATC CTT CCT					
R K N V I D P P I Y A R H I R I L P					
1575	1584	1593	1602	1611	1620
TGG TCC TGG TAC GGG AGG ATC ACA TTG GCG TCA GAG CTG CTG GGC TGC ACA GAG					
W S W Y G R I T L A S E L L G C T E					
1629	1638	1647	1656	1665	1674
GAG GAA TGA GTG GAG GCT ACA TTT CAC AAC CGT CTT CCC TAT TTG GGT AAA AGT					
E E * G E A T F H N R L P Y L G K S					
1683	1692	1701	1710	1719	1728
ATC TCC ATG GAA TGA ACT GTG TAA AAT CTG TAG GAA ACT GAA TGG TTT TTT TTT					
I S M E * T V * N L * E T E W F F F					
1737	1746	1755	1764	1773	
TTT TCA TGA AAA AGT GGT CAA ATT ATG GTA GGC AAC TAA CGG TGT TTT TAC C B'					
F S * K S G Q I M V G N * R C F Y					

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Figure 5

10	20	30	40	50	60
GACAGATGGC	CATGGATTCA	GATAAATTTG	CAAAGAAAAA	TGCGAGTCAC	TGGTGTATT
70	80	90	100	110	120
ACCCAAGGAG	CAAAAAGGAT	TGGAAGCCCA	GAGTACATAA	AATCCTACAA	AATTGCCTAC
130	140	150	160	170	180
AGCAATGACG	GGAGACCTG	GGCAATGTAC	AAAGTAAAAG	GCACCAATGA	AGAGATGGTC
190	200	210	220	230	240
TTTCGTGGAA	ATGTTGATAA	CAACACACCA	TATGCTAATT	CTTTCACACC	CCCAATCAAA
250	260	270	280	290	300
GCTCAGTATG	TAAGACTCTA	CCCCCAATT	TGTCGAAGGC	ATTGTACTTT	AAGAATGGAA
310	320	330	340	350	360
CTTCTTGGCT	GTGAGCTC...

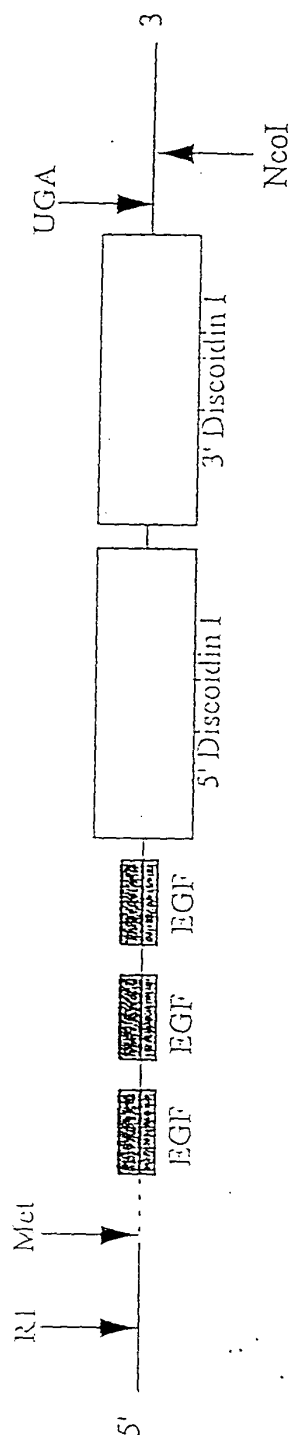
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Figure 6

m-del-1	MKHLVAAWLLVGLSLGVPQFGKGDICNPNPCENGGICLSGLADDSFSCEC	50
h-del-1	RS V D P VG	
m-del-1	PEGFAGPNCSSVVEVASDEEKPTSAGPCIPNPNCHNGGTCEISEAYRGDTF	100
h-del-1	D TD E T	
m-del-1	IGYVCKCPRGFNGIHCQHINECEAEPCPNNGGICTDLVANYSCCECPGEFM	150
h-del-1	V K	
m-del-1	GRNCQYKCSGHLGIEGGIISNQGITASSNHRALFGLQXWYPYARLNKKG	200
h-del-1	P T	
m-del-1	LINAWTAPENDRWP-WIQENLQKQRTVTCVITQGAKRIGSPEYIKSYRIA	249
h-del-1	NR +VTVG = "MIROZ" F	250
m-del-1	YSNDGKTWAMTKVKGTTNEEMVFRGNVDNNTPYANSFTPPIKAQYVRLYPQ	299
h-del-1	D I	300
m-del-1	ICRRHCTLRMELLGCELSGCSEPLGMKSGHIQDYQITASSVFRTLNMDMF	349
h-del-1	V I	350
m-del-1	TWEPRKARLDKQGVNAWTSCHNDQSQWLQVDLLVPTKVTGIIITQGAKDF	399
h-del-1	X X	400
m-del-1	GHVQFVGSYKLAYSNDGERWAWHQDEKQRKDKVFOGNFDNDTHPKNVIDP	449
h-del-1	T X X	450
m-del-1	PIYARFIRILPWSWYGRITLRSELLGCAEEE	480
h-del-1	H A T	481

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PROTEIN DOMAINS OF HUMAN DEL-1



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Figure 7

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Figure 8

1 10 20 30 40 50 60 70
N- CSTQLGMEGGATADSQISASVVMGFMGLQPWGPRLARLYPTGIVARWHSNYD-SRPWTQVNLRRMEV
** * * * * *
N- CSGPLGIEGGIISNQQTASSTHPALFGLQKWPYAPLAKKGLINGMTAAENDRGNRWIQINLQRKMEV
1 10 20 30 40 50 60 70
71 80 90 100 110 120 130 140
SGVMTQGASPRAGRAEVLNTFKVAYSIDG-RREFIQDESGGDKEFLGNLNNSLAVNMFNPTLEAQYIRL
** * * * * *
TGVITQGAIRIGSPETKFKYRIAYSNDGKTYAMTKVKGTHNEMVFRGNLHRTFFANSFTPPIRAQYVRL
71 80 90 100 110 120 130 140
141 150 160 170 180 190 200 210
YFVVSCHPGCTLRFFELIGCELHGCLPLGLKQNTIPDSQMSASSSYNTWNLPAFGWYPHLGRLENQGNRA
** * * * * *
YFQVCRPHCTLRMELLGCELSCGSEPLGKSGHIQDYQITASSIFRTLAGMFTWEPRARLDKQGNAR
141 150 160 170 180 190 200 210
211 220 230 240 250 260 270 280
WTAQSNSAKEWLQVDLGTQRTGITTQCAPDFGHIQYVESYRVVHSDDGVMQTVY--EDQGSSNVFQGN
** * * * * *
WTSCHNDQSQWLQVXLLVPTKVTGITTQGAIDKGVQFVGSYKLAYSDGHRWTVXQDERQKDRVXQGN
211 220 230 240 250 260 270 280
281 290 300 310 320
LNNSHKRNIFERCPFMARVVEVLVPSWHNPTLRLELLGC* -C
** * * * * *
FINDTHPRNVIDPPITVARIPLPWSWYGRITLASELLGCT -C
281 290 300 310 320

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Figure 9

PUTATIVE SIGNAL SEQUENCE OF HUMAN DEL-1

MKRSVAVWLLVGLSLGVPOFGKGDI...

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Figure 10

EGF-like Domains of hu Del-1

1)	CDPNPCENGGGICLPGLAVG-----SFSCECPDGFTDPNCS	SVVEVASDEEEPTSAGP
2)	CTPNPCHNGGTCEISEAYRGDFFIGYVCKCPRGFNGIHQ	HNINE
3)	CEVEPCRNNGGICTDLVA-----NYSCECPGEFMGRNCQ	YK
CONSENSUS	C---PC-NGG-C-----Y-C-C--GY-G--C-	
EGF DOMAIN		

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Figure 11

5'	-GT	GAT	ATT	TGT	GAT	CCC	AAT	CCA	TGT	GAA	AAT	GGA	GGT	ATC	TGT	TTG	CCA	GGA	5'
	X	D	I	C	D	P	N	P	C	E	N	G	G	I	C	L	P	G	
	TTG	GCT	GTA	GGT	TCC	TTT	TCC	TGT	GAG	TGT	CCA	GAT	GGC	TTC	ACA	GAC	CCC	AAC	
	L	A	V	G	S	F	S	C	E	C	P	D	G	F	T	D	P	N	
	TGT	TCT	AGT	GTT	GTG	GAG	GTT	GGT	CCC	TGC	ACT	CCT	AAT	CCA	TGC	CAT	AAT	GGA	
	C	S	S	V	V	E	V	G	P	C	T	P	N	P	C	H	N	G	
	GGA	ACC	TGT	GAA	ATA	AGT	GAA	GCA	TAC	CGA	GGG	GAT	ACA	TTC	ATA	GGC	TAT	GTT	
	G	T	C	E	I	S	E	A	Y	R	G	D	T	F	I	G	Y	V	
	TGT	AAA	TGT	CCC	CGA	GGA	TTT	AAT	GGG	ATT	CAC	TGT	CAG	CAC	AAC	ATA	AAT	GAA	
	C	K	C	P	R	G	F	N	G	I	H	C	Q	H	N	I	N	E	
	TGC	GAA	GTT	GAG	CCT	TGC	AAA	AAT	GGT	GGA	ATA	TGT	AGA	G	3'				
	C	E	V	E	P	C	K	N	G	G	I	C	T						

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Figure 12-B

10	20	30	40	50	60
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CGCGCCTCGC CTACTGTGCC CTCGCTACG ACCCCGGACC AGCCCAGGTC ACGTCCGTGA 540

BspHI

GAAGGGATCA TGAAGCACTT GGTAGCAGCC TGGCTTTTGG TTGGAATCAG CCTCGGGGTG 600
M K H L V A A W L L V G L S L G V

CCCCAGTTGG GCAAGGTGA CATTTCGAAC CCGAACCCCT GTGAAAATGG TGGCATCTGT 660
P Q F G N G D I C N P N P C E N G G I C

BspMI

CTGTCAGGAC TGGCTGATGA TTCCTTTTCC TGTGAGTGTC CAGAAGGCTT CGCAGGTCCG 720
L S G L A D D S F S C E C P E G F A G P

BspMI

AACTGCTCTA GTGTTGTGGA GGTTCATCA GATGAAGAAA AGCCTACTTC AGCAGGTCCC 780
N C S S V V E V A S D E E K P T S A G P

TGCATCCCTA ACCCATGCCA TAACGGAGGA ACCTGTGAGA TAAGCGAAGC CTATCGAGGA 840
C I P N P C H N G G T C E I S E A Y R G

GACACATTCA TAGGCTATGT TTGTAATGT CCTCGGGGAT TTAATGGGAT TCACTGTCAG 900
D T F I G Y V C K C P R G F N G I H C Q

CACAAATATA ATGAATGTGA AGCTGAGCCT TGCAGAAAATG GCGGAATATG TACCGACCTT 960
H N I N E C E A E P C R N G G I C T D L

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Figure 12c

10	20	30	40	50	60
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

BsmI

GTTGCTAACT ACTCTTGTGA ATGCCCAGGA GAATTTATGG GACGAAATTG TCAATATAAA 1020
V A N Y S C E C P G E F M G R N C Q Y K

TGCTCTGGGC ACTTGGGAAT CGAAGGTGGG ATCATATCTA ATCAGCAAAT CACAGCTTCA 1080
C S G H L G I E G G I I S N Q Q I T A S

SacI
Ecl1136II

TCTAATCACC GAGCTCTTTT TGGACTCCAG AAGTGGTATC CCTACTATGC TAGACTTAAT 1140
S N H R A L F G L Q K W Y P Y Y A R L N

NcoI
MscI
Bali

PvuII

AAGAAGGGCC TTATAAATGC CTGGACAGCT GCTGAAATG ACAGATGGCC ATGGATTCAG 1200
K K G L I N A W T A A E N D R W P W I Q

GTAACAGTGG GATGAGACAA ATCCATTGCC CAAATTATCA GAATCATTAT AGAAGTAGGT 1260
V T V G

TAGGGAGAAT TGGCTGTGAT TCTTTCTCAT GGTAAATG TGATTAGTT CAGAATTAAC - 1320

ATGGTTGGAA ACTCTAFAAA ATGTGGAAAA CAGGAACATT CTATGTCTGA AATCTGAAA 1380

ATAGCATCAA GATGAAAACA TTCTTTAGTC ATAAATATAC TCTTTTAAGT TATAGTAGAG 1440

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Figure 12D

10	20	30	40	50	60
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

BglIII

AAAAAGATCT TATCATTTCA TAAGTGGACT TTTGGGATAG CATTGGAAAT GTAAATGAAA 1500

SspI

TAAATACCTA ATTGAAAAAA GTTATTCTA AAGTGTTAAT ATTTAGCAAC AGATTCAGAG 1560

ACAAGAAAGT AACAAATTCAA TCTGTGTATT TTTGTGAGA AATAGTTTCC CATGTGCAAA 1620

FspI

BspHI

PstI

TATAAAGTGC GCATCATATC ATGATAATAT CCAACTGTCT GCAGAACTCC CTTTCATAAA 1680

TGAGAGAATT TTAATTCATA GTGCCTTATA TCCTCATCAG CCATCTGACT TTRACTACAGA 1740

NsiI

AGAAAACAAT GAAATGATGC ATTAAGTGCT TTGCTAGAAG AAACATCATA GCAAAGCTGA - 1800

XhoI

HindIII

PaeR7I

TAGCCACAT TCTGTGCANN NAAGCTTCCA GAGCACTCGA GAAAAGCAG AATGAGATG 1860

BclI

TTTATGAAA ACCGAAAAGA TAATCTGATT TCTGTGAAAT ATACTTTTGA TCATGTGGTT 1920

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Figure 12E

10	20	30	40	50	60
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CTTTAAGATA GTCACATAACA AGTCATTAGT AGCAGATACC AAATGGGAGA AAATTTCCAG 1930

Bst1107I

TATACTGAGG GTCAGGCAG TCATGCTGAA ACTACATGAG GTCAGGAAG TTTTGAAATA 2040

AGGTGATTTT GGAAGGATAC CTTCAACTGG CCTAGATTTT CAAGAAACAG TGTATCAAC 2100

AGCCAAACAT GAGAATCTAG CTAACAGCAT TTAGAAACC AGAACTAAGA GTGTTACTGG 2150

DraI

GGAATTGCAT TTAAATCCAG TATGAGAGTT TGCAATGCC GTATTCTTCT AAGGGGTTTC 2220

NcoI

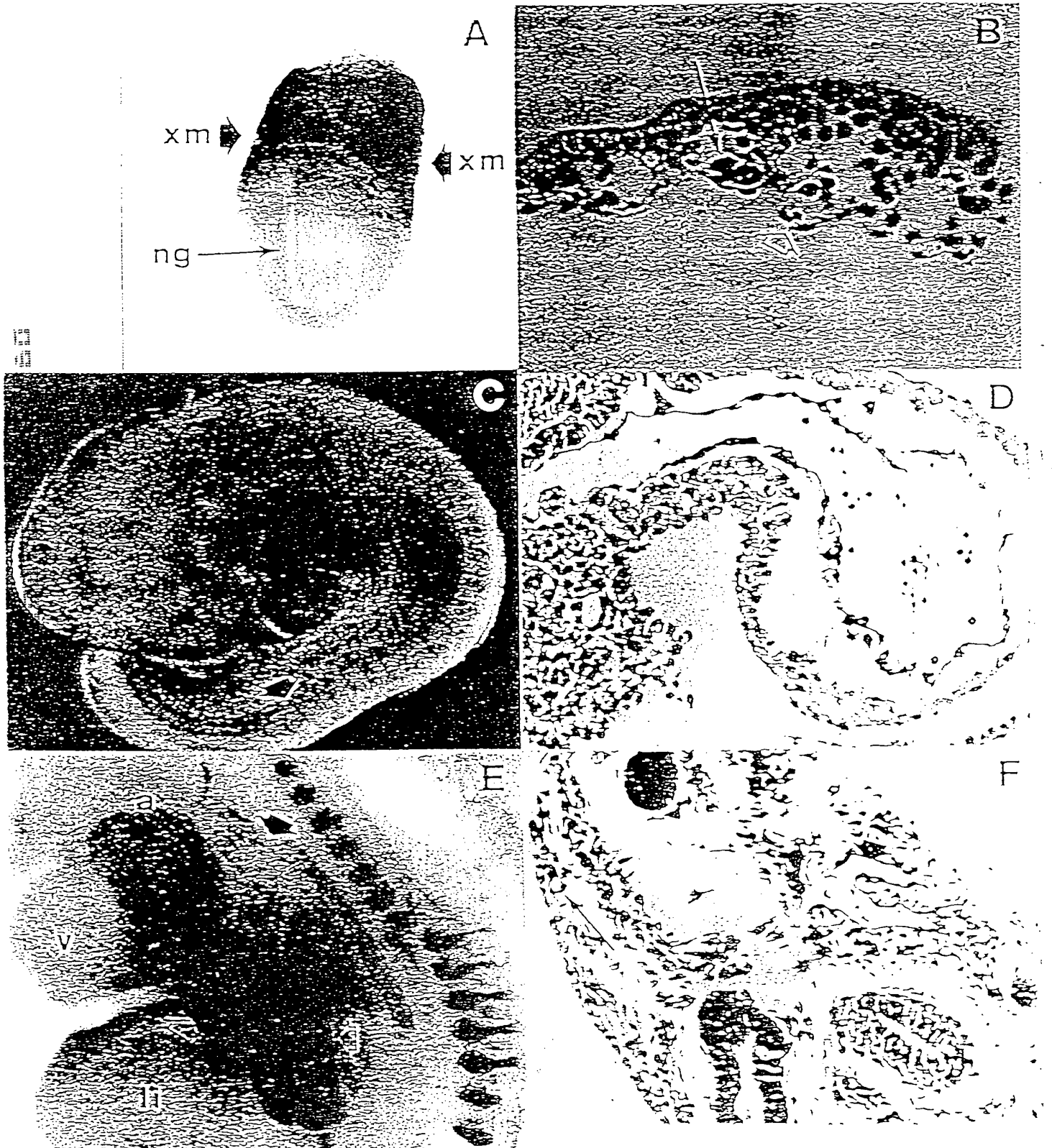
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EcoRI

ACTATAATTT GAATAAAGC CGGAATTC 2305

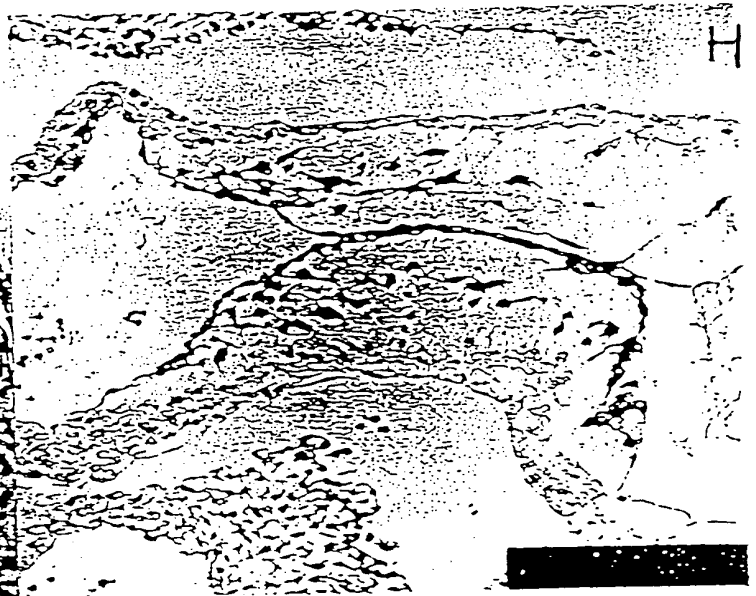
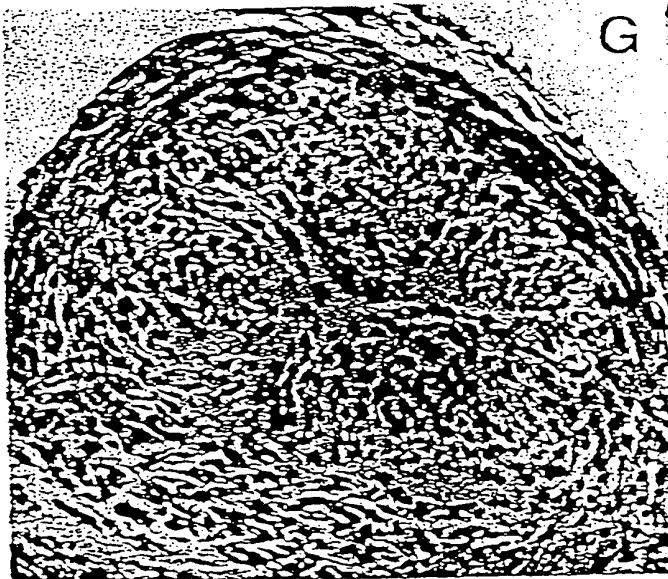
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Figure 13 A - 13 F



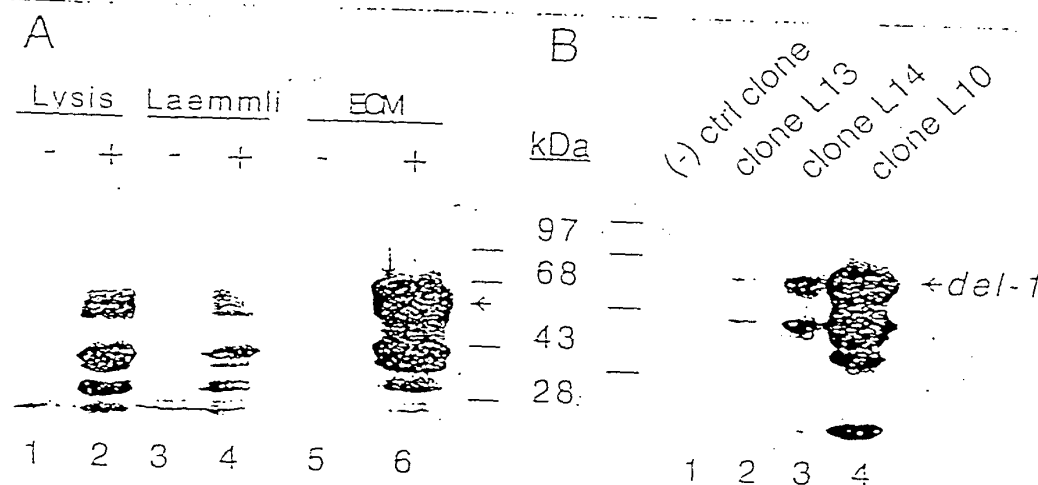
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Figure 13G and 13H



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Figure 14A and 14B



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Figure 15A

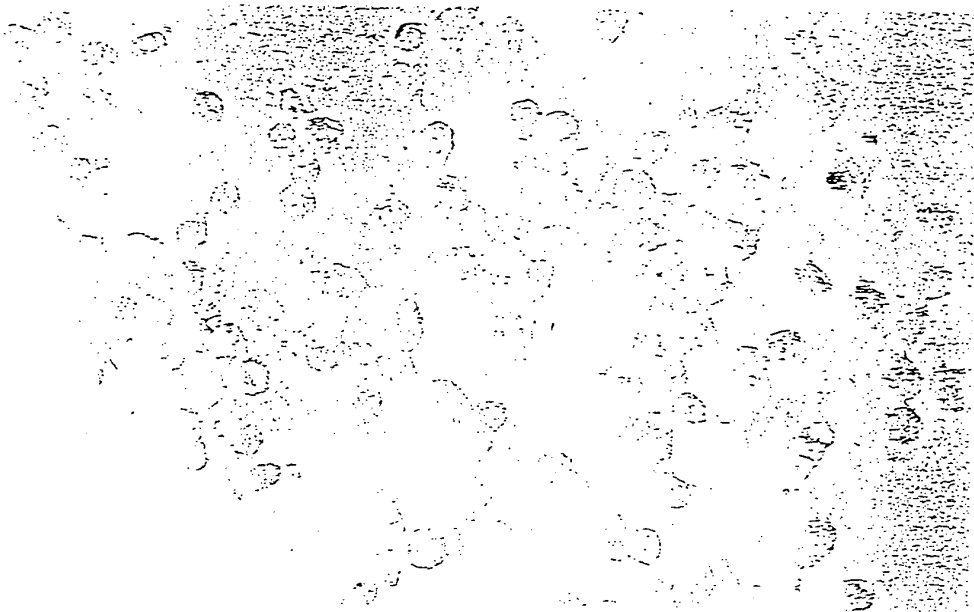
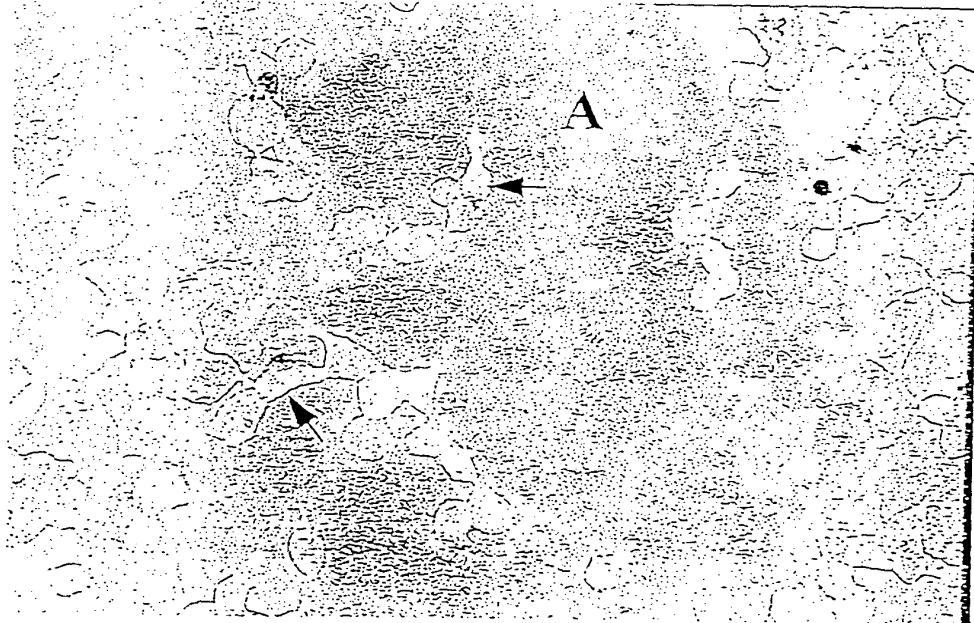
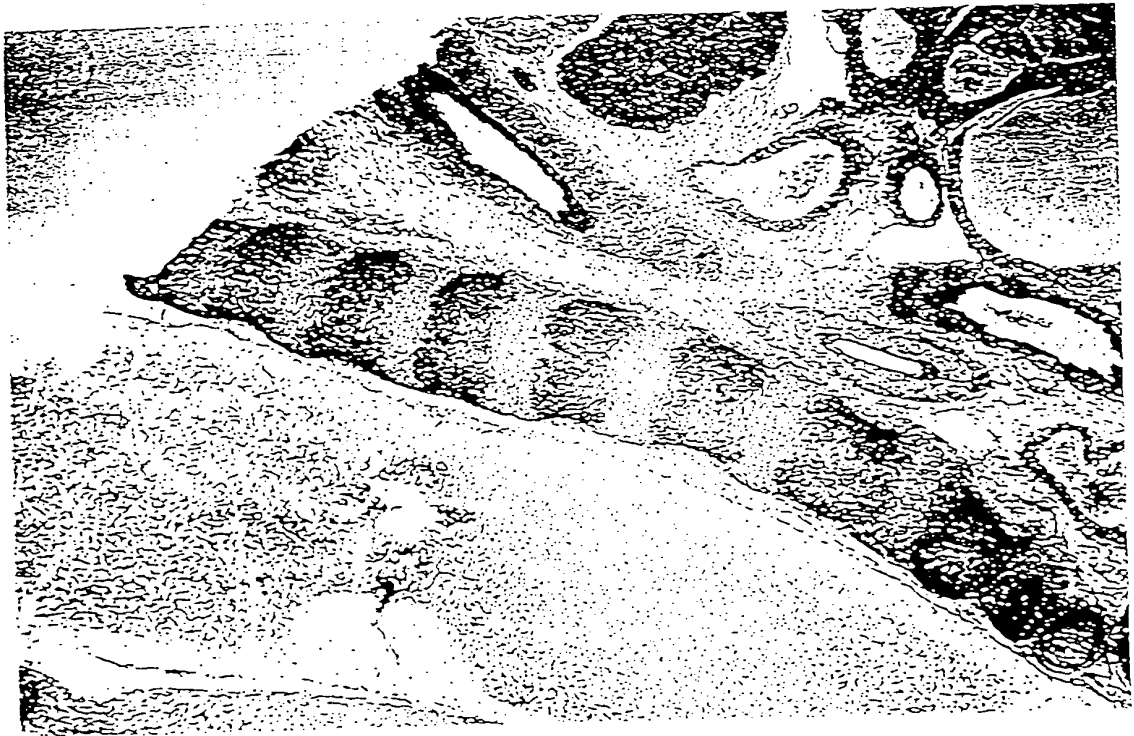


Figure 15B

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Figure 16



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Figure 16

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Figure 17A

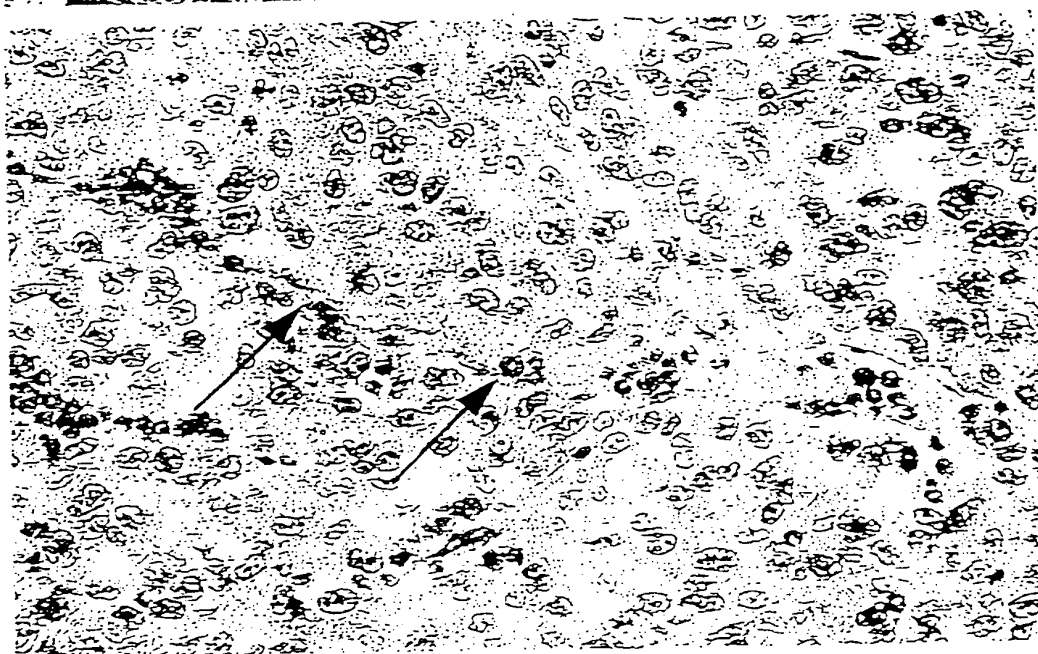
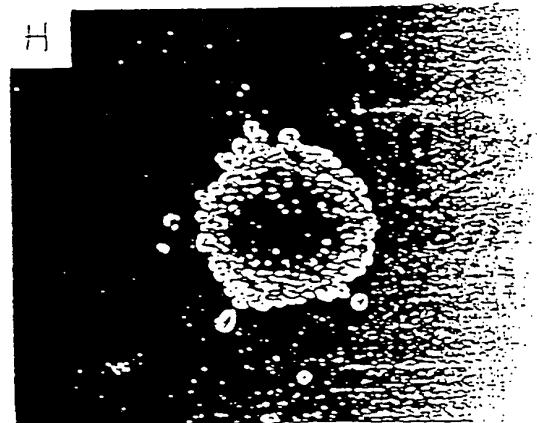
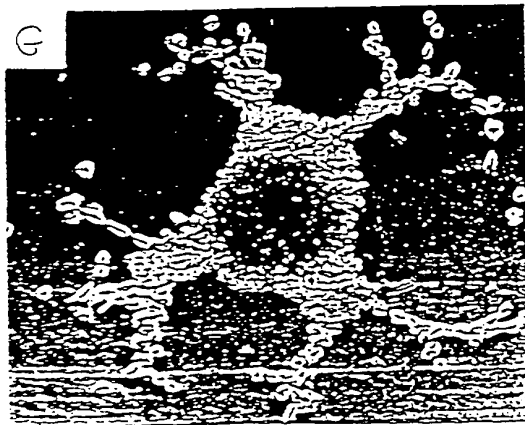
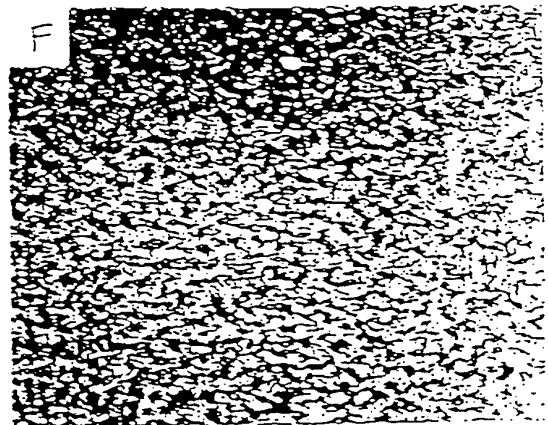
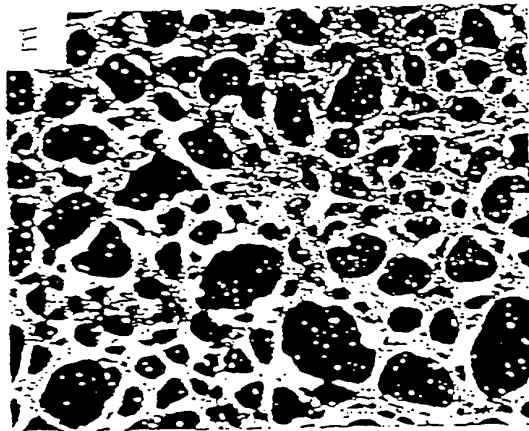
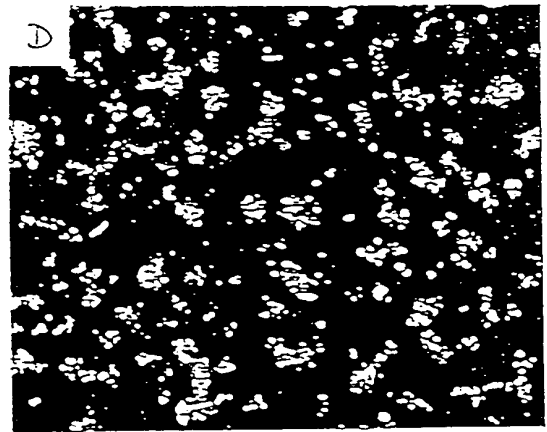
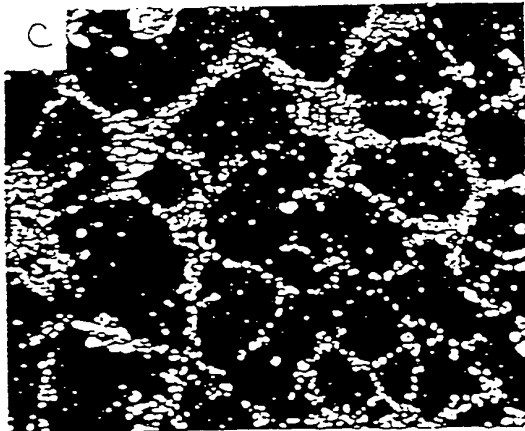
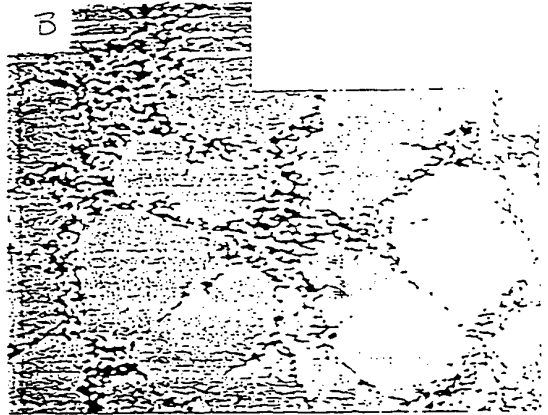
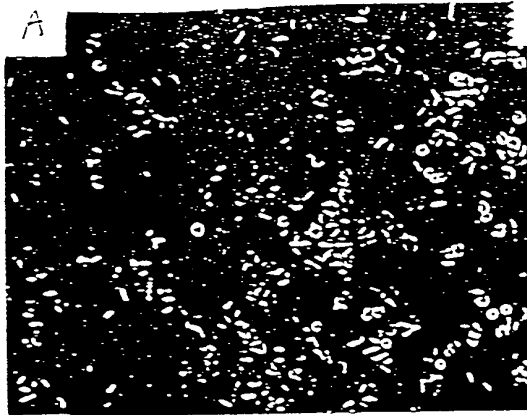


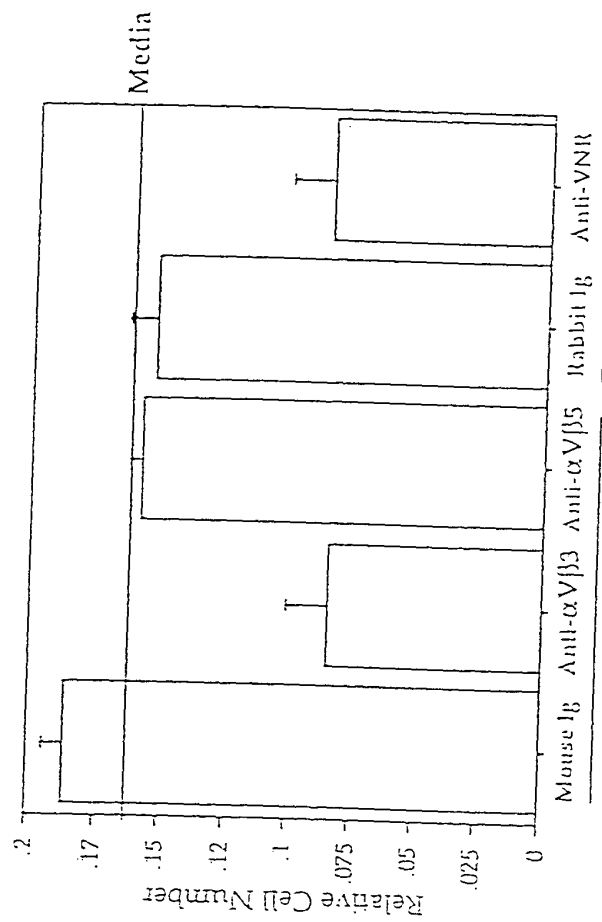
Figure 17B

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Figure 18 A-18H



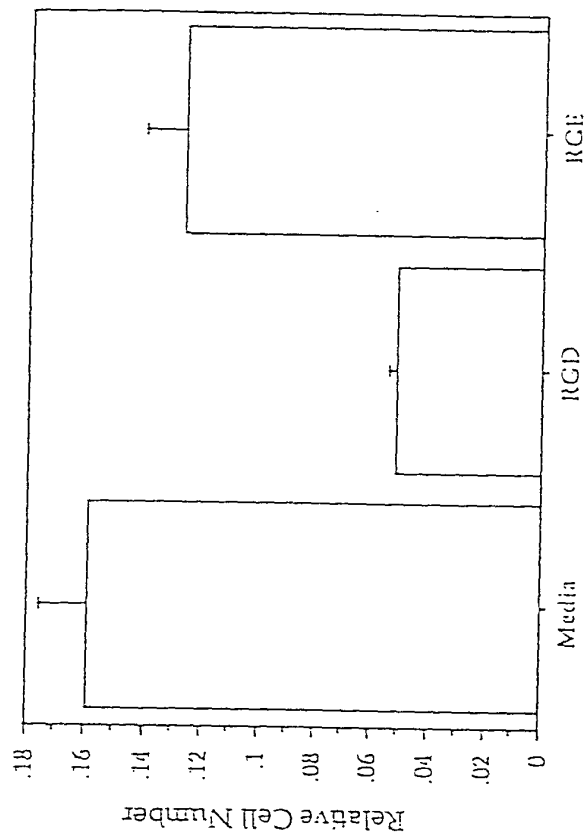
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Figure 19



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Figure 20



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Figure 21A

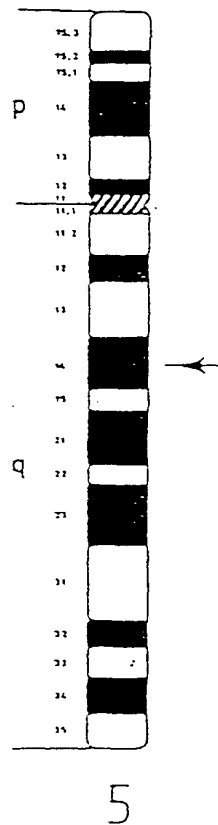


Figure 21B

